

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 3, 2003, 13:01:31 ; Search time 5.65217 Seconds
(without alignments)
170.084 Million cell updates/sec

Title: US-09-801-784A-36
Perfect score: 50
Sequence: 1 PSVAALTYSP 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

c-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	88.0	171	2 A41467	fimbrial protein C
2	40	80.0	170	1 YQECCL	CFAI fimbrial prot
3	40	80.0	170	2 B56617	colonization facto
4	38	76.0	2344	2 S64740	genome polypeptide
5	36	72.0	234	2 S22134	capsid protein - r
6	36	72.0	336	2 S27901	site-specific DNA-
7	36	72.0	336	2 T17743	site-specific DNA-
8	36	72.0	377	1 MFNZP2	matrix protein - p
9	36	72.0	427	2 T41257	hypothetical prote
10	36	72.0	537	2 S62749	A-alpha X protein
11	35	70.0	251	2 A55523	hypothetical prote
12	35	70.0	280	2 S72748	Bl177 F3 136 prote
13	35	70.0	374	1 DEHNAS	alcohol dehydrogen
14	35	70.0	374	1 A56436	hypothetical prote
15	35	70.0	424	2 T33663	hypothetical prote
16	35	70.0	444	2 S64912	probable membrane
17	35	70.0	486	2 S74319	RTG3 protein - yea
18	35	70.0	804	2 H75549	glycogen debranchi
19	35	70.0	963	2 S45167	chitin synthase (E
20	35	70.0	2344	2 S55399	genome polypeptide
21	34	68.0	331	2 G75035	iron (III) abc tra
22	34	68.0	350	2 T40466	probable acetyltra
23	34	68.0	460	2 B82549	hypothetical prote
24	34	68.0	540	1 CYHUCR	naturietic peptid
25	34	68.0	570	2 T33714	probable kexin (EC
26	34	68.0	610	2 T35797	secreted chitinase
27	34	68.0	699	2 E87803	protein bli-4E (Im
28	34	68.0	730	2 F87803	protein bli-4B (Im
29	34	68.0	942	2 D87803	protein bli-4D (Im

30	34	68.0	1877	2 T40550	probable phosphati
31	34	68.0	2016	2 A38195	sodium channel pro
32	33	66.0	115	2 S75392	hypothetical prote
33	33	66.0	156	2 C82971	conserved hypochet
34	33	66.0	181	2 T52409	ucalycanin II (Im
35	33	66.0	193	2 B90157	hypothetical prote
36	33	66.0	199	2 T52410	blue copper-bindin
37	33	66.0	201	2 T52408	blue copper-bindin
38	33	66.0	202	2 T01605	phytoeyanin At2344
39	33	66.0	225	2 H75538	conserved hypochet
40	33	66.0	310	2 T43158	probable GTP-bindi
41	33	66.0	314	2 T43289	probable GTP-bindi
42	33	66.0	333	2 G95209	hypothetical prote
43	33	66.0	336	2 B95015	glycoproteinase fa
44	33	66.0	336	2 C97888	O-sialoglycoprotei
45	33	66.0	369	1 MFNZLA	matrix protein - L

ALIGNMENTS

RESULT 1
A41467
fimbrial protein csaA - Escherichia coli plasmid pEU405
N.Alternate names: Csl pilus major subunit
C.Species: Escherichia coli
C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 26-Aug-1999
C.Accession: A41467; S19003
R.Repert-Casal, U.; Swartley, J.S.; Scott, J.R.
R.Perez-Casal, U.; Swartley, J.S.; Scott, J.R.
Interf. Immun. 58, 3594-3600, 1990
A.Title: Gene encoding the major subunit of Csl pili of human enterotoxigenic Escherichia coli
A.Reference number: A41467; MUID:91034170; PMID:1977705
A.Accession: A41467
A.Molecule type: DNA
A.Residues: 1-171 <PER>
A.Residues: 1-171 <PER>
A.Cross-references: GB:M07148; GB:M58550; NID:9145573; PIDN:AAA23596.1; PID:9145574
R.Jordt, B.J.A.M.; van Vliet, A.H.M.; Willems, G.A.; van der Zeijst, B.A.M.; Gaaststra, W.
FEMS Microbiol. Lett. 80, 265-270, 1991
A.Title: Analysis of the first two genes of the Csl fimbrial operon in human enterotoxigenic Escherichia coli
A.Reference number: S19002
A.Accession: S19003
A.Status: Preliminary
A.Molecule type: DNA
A.Residues: 1-171 <JOR>
A.Cross-references: EMBL:X62879; NID:911169; PIDN:CAA44673.1; PID:911171
C.Genetics:
A.Gene: csaA
A.Genome: Plasmid
C.Superfamily: CFAI fimbrial protein

Query Match 88.0%; Score 44; DB 2; Length 171;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSVAALTYSP 10
[:::|||||]
DB 49 PMSVAALTYSP 58

RESULT 2
YQECCL
CFAI fimbrial protein precursor - Escherichia coli
N.Alternate names: CFAI pili; colonization factor antigen I (CFAI)
C.Species: Escherichia coli
C.Date: 14-Nov-1983 #sequence_revision 30-Jun-1991 #text_change 15-Nov-1996
C.Accession: A30589; A03495; A43831
R.Katralainen, T.K.; Evans, D.G.; So, M.; Lee, C.H.
Interf. Immun. 57, 1126-1130, 1989
A.Title: Molecular cloning and nucleotide sequence of the colonization factor antigen I
A.Reference number: A30589; MUID:89173309; PMID:2564374
A.Molecule type: DNA
A.Residues: 1-170 <KAR>

R;Klemm, P.
 Eur. J. Biochem. 124, 339-348, 1982
 A;Title: Primary structure of the CFAI fimbrial protein from human enterotoxigenic Esche
 A;Reference number: A03495; MUID:62235736; PMID:6124420
 A;Accession: A03495
 A;Molecule type: DNA
 A;Residues: 24-75, 'N', 77-96, 'A', 98-170 <KLE>
 A;Experimental source: strain H10407
 R;Cassels, F.J.; Deal, C.D.; Reid, R.H.; Jarboe, D.L.; Nauss, J.L.; Carter, J.M.; Boedek
 Infect. Immun. 60, 2174-2181, 1992
 A;Title: Analysis of Escherichia coli colonization factor antigen I linear B-cell epitop
 A;Reference number: A4381; MUID:92267624; PMID:13375193
 A;Accession: A4381
 A;Molecule type: protein
 A;Residues: 24-170 <CAS>
 A;Experimental source: strain H10407
 A;Note: sequence extracted from NCBI backbone (NCBIP:104220)
 C;Comment: The CFAI fimbriae are rather rigid, thread-like filaments of 0.5-1 micrometer
 tical protein subunits.
 C;Superfamily: CFAI fimbrial protein
 C;Keywords: fimbria
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-170/Product: CFAI fimbrial protein #status experimental <MAT>
 Query Match 80.0%; Score 40; DB 1; Length 170;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 PSAVALTYSP 10
 Db 49 PSAVKLAYSP 58
 ||||| ||||
 RESULT 3
 B56617
 colonization factor antigen I precursor - Escherichia coli plasmid NTP113
 C;Species: Escherichia coli
 C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 03-May-1996
 C;Accession: B56617
 R;Jordi, B.J.; Willshaw, G.A.; van der Zeijst, B.A.; Gastra, W.
 DNA Seq. 2, 257-263, 1992
 A;Title: The complete nucleotide sequence of region 1 of the CFA/I fimbrial operon of hu
 A;Reference number: A56617; MUID:92329981; PMID:1327212
 A;Accession: B56617
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-170 <JOR>
 A;Experimental source: enterotoxigenic strain, CFA/I-ST plasmid NTP113
 A;Note: sequence inconsistent with nucleotide translation
 A;Note: sequence extracted from NCBI backbone (NCBIN:108960, NCBIP:108970)
 C;Genetics:
 A;Gene: cfab
 A;Genome: plasmid
 C;Superfamily: CFAI fimbrial protein
 Query Match 80.0%; Score 40; DB 2; Length 170;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 PSAVALTYSP 10
 Db 49 PSAVKLAYSP 58
 ||||| ||||
 RESULT 4
 S64740
 genome polyprotein - rabbit hemorrhagic disease virus (isolate AST/89)
 N;Contains: VP60 protein
 C;Species: rabbit hemorrhagic disease virus
 A;Variety: isolate AST/89
 C;Date: 12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
 C;Accession: S64740; S46944; S49018; S65012
 R;Casals, R.; Martin-Alonso, J.; Boga, J.; Parra, F.

submitted to the EMBL Data Library, May 1995
 A;Description: Genomic organization of rabbit hemorrhagic disease virus determined by di
 A;Reference number: S64740
 A;Accession: S64740
 A;Molecule type: genomic RNA
 A;Residues: 1-2344 <CAS>
 A;Cross-references: EMBL:Z49271; NID:g1182032; PIDN:CAA89265.1; PID:g1150552
 A;Experimental source: isolate AST/89
 R;Boga, J.; Casals, R.; Marin, M.; Martin-Alonso, J.; Carmenes, R.; Prieto, M.; Parra, F
 submitted to the EMBL Data Library, July 1993
 A;Description: Molecular cloning, sequence and expression of the capsid protein gene fro
 A;Reference number: S46944
 A;Accession: S46944
 A;Molecule type: Genomic RNA
 A;Residues: 1650-2344 <BOG>
 A;Cross-references: EMBL:Z24757; NID:g515622; PIDN:CAA80881.1; PID:g515623
 A;Experimental source: isolate AST/89
 R;Parra, F.; Boga, J.A.; Marin, M.S.; Casals, R.
 Virus Res. 27, 219-228, 1993
 A;Title: The amino terminal sequence of VP60 from rabbit hemorrhagic disease virus suppo
 A;Reference number: S49018; MUID:93255896; PMID:8488721
 A;Accession: S49018
 A;Molecule type: genomic RNA
 A;Residues: 1650-1796 <PAR>
 A;Cross-references: EMBL:Z24757
 A;Experimental source: isolate AST/89
 A;Accession: S65012
 A;Molecule type: protein
 A;Residues: 1767-1779;1875-1877, 'X', 1879-1881;1936-1938, 'X', 1940 1941 <PAW>
 C;Superfamily: rabbit calicivirus RNA-directed RNA polymerase
 C;Keywords: blocked amino end; polyprotein
 Query Match 76.0%; Score 38; DB 2; Length 2344;
 Best Local Similarity 70.0%; Pred. No. 64;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSAVALTYSP 10
 Db 2194 PSANAITYTP 2203
 ||||| |||||
 RESULT 5
 S22134
 capsid protein - rabbit hemorrhagic disease virus (fragment)
 C;Species: rabbit hemorrhagic disease virus
 C;Date: 20-Feb-1995 #sequence_revision 26-Apr-1996 #text_change 18-Jun-1999
 C;Accession: S22134
 R;Carter, M.
 submitted to the EMBL Data Library, November 1991
 A;Reference number: S22134
 A;Accession: S22134
 A;Molecule type: genomic RNA
 A;Residues: 1-234 <CAR>
 A;Cross-references: EMBL:Z11535; NID:g61803; PIDN:CAA77633.1; PID:g61804
 A;Experimental source: strain V-351
 C;Superfamily: rabbit calicivirus RNA-directed RNA polymerase
 C;Keywords: capsid protein
 Query Match 72.0%; Score 36; DB 2; Length 234;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSAVALTYSP 10
 Db 84 PNASAITYP 93
 ||||| |||||
 RESULT 6
 S27901
 site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) CviA11
 N;Alternate names: DNA adenine methyltransferase CviA11
 C;Species: Chlorrella virus PBCV-1
 C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

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C:\Accession: S35442; S27901
R.Zhang, Y.; Nelson, M.; Nierfeldt, J.W.; Burbank, D.E.; Van Etten, J.L.
Nucleic Acids Res. 20, 5351-5356, 1992
A.Title: Characterization of Chlorella virus PBCV-1
A.Reference number: S35442; MUID:93065201; PMID:1437552
A.Accession: S35442
A.Molecule type: DNA
A.Residues: 1-326 <ETT>
A.Cross-references: EMBL:M86639; NID:G323316; PID:G323317
C:Superfamily: site-specific methyltransferase (adenine-specific) NlaIII
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match      72.0%; Score 36; DB 2; Length 326;
Best local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 PSAVALTYSP 10
      | | | | |
Db      95 PGFVLTLYSP 104

RESULT 7
117743
Site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) - Chlorella virus PBCV-1
Accession: T17743
C:Accession: T17743
R.Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A.Reference number: Z18806
A.Accession: T17743
A.Status: preliminary; translated from GR/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-326 <GRA>
A.Cross-references: EMBL:U42580; NID:G4028896; PID:AA096619.1
C:Genetics:
A>Note: A251R
C:Superfamily: site-specific methyltransferase (adenine-specific) NlaIII
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match      72.0%; Score 36; DB 2; Length 326;
Best local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 PSAVALTYSP 10
      | | | | |
Db      95 PGFVLTLYSP 104

RESULT 8
MENP2
Matrix protein - parainfluenza virus type 2
Accession: A36421; S1661
R.Kawano, M.; Bando, H.; Ohgimoto, S.; Okamoto, K.; Kondo, K.; Tsurudome, M.; Nishio, M.
Virology 179, 857-861, 1990
A.Title: Complete nucleotide sequence of the matrix gene of human parainfluenza type 2 virus
A.Reference number: A36421; MUID:91049454; PMID:2173264
A.Accession: A36421
A.Molecule type: genomic RNA
A.Residues: 1-317 <KAN>
A.Cross-references: GB:M67734; NID:G332730; PID:AAA46862.1; PID:G332731
R.Kawano, M.; Okamoto, K.; Bando, H.; Kondo, K.; Tsurudome, M.; Komada, H.; Nishio, M.;
Nucleic Acids Res. 19, 2719-2746, 1991
A.Title: Characterizations of the human parainfluenza type 2 virus gene encoding the L protein
A.Reference number: S16659; MUID:91252221; PMID:1645865
A.Accession: S16661
A.Molecule type: genomic RNA
A.Residues: 1-317 <KAN>
A.Cross-references: EMBL:X57559; NID:G61985; PID:CAA40785.1; PID:G61988
A.Experimental source: strain Toshiba
C:Genetics:

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A:Superfamily: parainfluenza virus matrix protein
C:Keywords: matrix protein

Query Match          72.0%; Score 36; DB 1; Length 377;
Best Local Similarity 60.0%; Pred. No. 25;
Matches      6; Conservative    3; Mismatches     1; Indels     0; Gaps     0;

OY      1 PSAVALTYSP 10
        |||::|||
Db       170 PTFVSAITYSP 179

RESULT 9
T41257
Hypotheical protein SPCC285.11 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T41257
R:Seeger, K.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21981
A:Accession: T41257
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-427 <SEE>
A:Cross-references: EMBL:AL031545; PIDN:CAA20850.1; GSPDB:GN00068; SPDB:SPCC285.11
C:Genetics:
A:Experimental source: strain 972h-; cosmid c285
C:Genetics:
A:Gene: SPDB:SPCC285.11
A:Map position: 3
A:Introns: 36/3

Query Match          72.0%; Score 36; DB 2; Length 427;
Best Local Similarity 70.0%; Pred. No. 28;
Matches      7; Conservative    1; Mismatches     2; Indels     0; Gaps     0;

OY      1 PSAVALTYSP 10
        ||||:||||
Db       203 PSAVLWMTSP 212

RESULT 10
S62749
A-alpha X protein (allele 3) - bracket fungus (Schizophyllum commune)
C:Species: Schizophyllum commune
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S62749
R:Matton, A.L.; Bartholomew, K.A.; Wu, J.; Yang, H.; Novotny, C.P.; Ullrich, R.C.
Curr. Genet. 29, 143-149, 1996
A>Title: The A-alpha mating-type locus of Schizophyllum commune: structure and function
A:Reference number: S62748; PMID:96418876; PMID:8821661
A:Accession: S62749
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-537 <MAR>
A:Cross-references: EMBL:U13943; NID:G537622; PIDN:AAB41338.1; PID:G537623
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1994
C:Genetics:
A:Introns: 21/3
C:Superfamily: A-alpha X protein

Query Match          72.0%; Score 36; DB 2; Length 537;
Best Local Similarity 80.0%; Pred. No. 35;
Matches      8; Conservative    0; Mismatches     2; Indels     0; Gaps     0;

OY      1 PSAVALTYSP 10
        |||::|||
Db       172 PSEVALTESP 181

RESULT 11
AS5523

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hypothetical protein (bphD 3' region) - Pseudomonas sp. (strain KKS102)
 C:Species: Pseudomonas sp.
 C:Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 11-Jan-2002
 C:Accession: A55523
 R:Kikuchi, Y.; Nagata, Y.; Hinata, M.; Kimbara, K.; Fukuda, M.; Yano, K.; Takagi, M.
 J. Bacteriol. 176, 1689-1694, 1994
 A:Title: Identification of the bphA4 gene encoding ferredoxin reductase involved in biophenol production in Pseudomonas sp. strain KKS102
 A:Reference number: A55523; MUID:94179104; PMID:8132464
 A:Accession: A55523
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-251 <KIK>
 A:Cross-references: GB:U07821; NID:9391830; PIDN:BAA04111.1; PID:G431769

Query Match 70.0%; Score 35; DB 2; Length 251;
 Best Local Similarity 60.0%; Pred. No. 26;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PSAVALTYSP 10
 I: : |||||
 DB 114 PAILLTYS 123

RESULT 12
 S72748
 B1177 F3 136 protein - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
 C:Accession: S72748
 R:Smith, D.R.; Robinson, K.
 submitted to the EMBL Data Library, November 1993
 A:Description: Mycobacterium leprae cosmid B1177.
 A:Reference number: S72694
 A:Accession: S72748
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <SMI>
 A:Cross-references: EMBL:U00011; NID:9466807; PIDN:AAA17112.1; PID:G466837
 C:Genetics:
 A:Start codon: GTG
 C:Superfamily: conserved hypothetical protein AF1561

Query Match 70.0%; Score 35; DB 2; Length 260;
 Best Local Similarity 70.0%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PSAVALTYSP 10
 I: : |||||
 DB 32 PTLVALGYSP 41

RESULT 13
 DEHUAS
 alcohol dehydrogenase (EC 1.1.1.1) 7 [validated] - human
 A:Alternate names: alcohol dehydrogenase mu chain [mismomer]; alcohol dehydrogenase sign
 N:Contains: retinol dehydrogenase (EC 1.1.1.105)
 C:Species: Homo sapiens (man)
 C:Date: 23-Mar-1995 #sequence_revision 08-Mar-1996 #text_change 15-Sep-2000
 C:Accession: A56878; A54018; A56083; S48667; JC2546; S48147; S21170
 R:Kedrisvili, N.Y.; Bosron, W.F.; Stone, C.L.; Hurley, T.D.; Peggs, C.F.; Thomasson, H.R.
 J. Biol. Chem. 270, 3625-3630, 1995
 A:Title: Expression and kinetic characterization of recombinant human stomach alcohol de
 A:Reference number: A55878; MUID:95181314; PMID:7876099
 A:Accession: A55878
 A:Molecule type: mRNA
 A:Residues: 1-374 <KED>
 A:Cross-references: GB:U09623; NID:9790523; PIDN:AAA82165.1; PID:G790524
 A:Note: parts of this sequence were determined by protein sequencing; the amino end of t
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor
 F:2-374/Product: long-chain alcohol dehydrogenase 7 #status experimental <MAT>
 F:32-365/Domain: long-chain alcohol dehydrogenase homology <LADH>
 J. Biol. Chem. 269, 15606-15612, 1994
 A:Title: The complete structure of human class IV alcohol dehydrogenase (retinol dehydro
 A:Reference number: A54018; MUID:94253145; PMID:8195208

A:Accession: A54018
 A:Molecule type: mRNA
 A:Residues: 1-374 <SAT>
 A:Cross-references: GB:U07821; NID:9499097; PIDN:AAA19002.1; PID:G499098
 R:Zgoncic-Knight, M.; Foglio, M.H.; Duester, G.
 J. Biol. Chem. 270, 4305-4311, 1995
 A:Title: Genomic structure and expression of the ADH7 gene encoding human class IV alcohol
 A:Reference number: A56083; MUID:95181413; PMID:7876191
 A:Accession: A56083
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-374 <ZGO>
 A:Cross-references: GB:U16286; GB:U16287; GB:U16288; GB:U16289; GB:U16290; GB:U16291; GB
 R:Yokoyama, S.; Matsuo, Y.; Ramsbotham, R.; Yokoyama, R.
 FEBS Lett. 351, 411-415, 1994
 A:Title: Molecular characterization of a class IV human alcohol dehydrogenase gene (ADH7)
 A:Reference number: S48667; MUID:94364515; PMID:8082805
 A:Accession: S48667
 A:Molecule type: DNA
 A:Residues: 1-107, 'E', 'I', '109-272, 'D', '274-286, 'V', '288-374 <YOKI>
 A:Cross-references: GB:U33179; NID:9516617
 A:Note: the authors translated the codon GAT (Asp) for residue 108 as Glu and GAA (Glu)
 A:Note: the sequence in GenBank entry HUMALDE, release 103 (PID:G516618) corresponds to
 R:Yokoyama, H.; Baraona, E.; Lieber, C.S.
 Biochem. Biophys. Res. Commun. 203, 219-224, 1994
 A:Title: Molecular cloning of human class IV alcohol dehydrogenase cDNA.
 A:Reference number: JC2546; MUID:94354804; PMID:8074657
 A:Accession: JC2546
 A:Molecule type: mRNA
 A:Residues: 2-374 <YOK2>
 A:Cross-references: GB:U33179; NID:9516617; PIDN:AAA59211.1; PID:G516618
 A:Experimental source: stomach
 R:Farres, J.; Moreno, A.; Crosas, B.; Peralba, J.M.; Allali-Hassani, A.; Hjelqvist, L.;
 Eur. J. Biochem. 224, 549-557, 1994
 A:Title: Alcohol dehydrogenase of class IV (sigma-sigma-ADH) from human stomach. cDNA se
 A:Reference number: S48147; MUID:95010033; PMID:7925371
 A:Accession: S48147
 A:Molecule type: mRNA
 A:Residues: 1-374 <PAR>
 A:Cross-references: EMBL:X76342; NID:9541674; PIDN:CAA53961.1; PID:G541676
 R:Pares, X.; Cederlund, E.; Moreno, A.; Saubi, N.; Hoeoeg, J.O.; Joernvall, H.
 FEBS Lett. 303, 69-72, 1992
 A:Title: Class IV alcohol dehydrogenase (the gastric enzyme). Structural analysis of hum
 ogenase class.
 A:Reference number: S21170; MUID:92275085; PMID:1592118
 A:Accession: S21170
 A:Molecule type: protein
 A:Residues: 12-18, 'XR', '21-41-46, '62-70, 'R', '72-77, 'X', '79, 'XXXXX', '85-86, 'X', '88-111, '135-137,
 R:Hurley, T.D.; Xie, P.
 submitted to the Brookhaven Protein Data Bank, June 1996
 A:Reference number: A65066; PDB:1AGN
 A:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 2-374
 C:Genetics:
 A:Gene: GDB:ADH7
 A:Cross-references: GDB:362911; OMIM:600086
 A:Map position: 4q23-q24
 A:Introns: 6/3; 40/3; 87/1; 116/2; 188/3; 275/3; 321/1; 367/2
 C:Complex: homodimer
 C:Function: <ADH>
 A:Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an
 C:Function: <RDH>
 A:Pathway: alcohol degradation
 A:Description: catalyzes the oxidation of retinol to retinal by NAD+
 A:Pathway: retinoic acid biosynthesis
 A:Note: retinoic acid regulates epithelial cell differentiation
 A:Note: abundant in stomach, eye, skin, thymus, and ovary
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidor
 F:2-374/Product: long-chain alcohol dehydrogenase 7 #status experimental <MAT>
 F:32-365/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F:194-223/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Gly) (in mature form) #status predicted

F:47,68,174/Binding site: zinc, catalytic (Cys, His, Cys) #status experimental
F:98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status experimental

Query Match

70.0%; Score 35; DB 1; Length 374;
Best Local Similarity Pred. No. 39;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10

Db 296 PSAAKMLTYDP 305

RESULT 14

A:56436

alcohol dehydrogenase (EC 1.1.1.1) IV - mouse

N:Alternate names: class IV alcohol dehydrogenase mu chain; class IV alcohol dehydrogenase

C:Species: retinol dehydrogenase (EC 1.1.1.105)

C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jun-1999

C:Accession: A56436

R:Zgoncic-Knight, M.; Ang, H.L.; Foglio, M.H.; Duester, G.

J. Biol. Chem. 270, 10868-10877, 1995

A:Title: Cloning of the mouse class IV alcohol dehydrogenase (retinol dehydrogenase) cDN

A:Reference number: A56436; MUID:95256239; PMID:7758026

A:Accession: A56436

A:Residues: 1-374 <ZGO>

A:Cross-references: GB:U20257; NID:g897584; PIDN:AAA76735.1; PID:g897585

C:Genetics:

A:Gene: Adh-3

C:Complex: homodimer

C:Function: <ADH>

A:Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an

C:Pathway: alcohol degradation

C:Function: <RDH>

A:Description: catalyzes the oxidation of retinol to retinal by NAD+

A:Pathway: retinoic acid biosynthesis

A>Note: retinoic acid regulates epithelial cell differentiation

A>Note: abundant in stomach, eye, skin, thymus, and ovary

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase

F:2-374/Product: alcohol dehydrogenase IV #status predicted <MAT>

F:35-365/Domain: long-chain alcohol dehydrogenase homology <LADH>

F:194-223/Region: beta-alpha-beta NAD nucleotide-binding fold

F:2/Modified site: acetylated amino end (Gly) (in mature form) #status predicted

F:47,68,174/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

F:98,101,104,112/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match

70.0%; Score 35; DB 1; Length 374;
Best Local Similarity Pred. No. 39;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10

Db 296 PSAAKMLTYDP 305

RESULT 15

T33663

hypothetical protein W04B5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T33663

R:Smith, A.; Gibson, A.

submitted to the EMBL Data Library, October 1998

A:Description: The sequence of C. elegans cosmid W04B5.

A:Reference number: Z21385

A:Accession: T33663

A:Status: preliminary; translated from GB/EMBL/DBD/J

A:Molecule type: DNA

A:Residues: 1-424 <SMI>

A:Cross-references: EMBL:AF100305; PIDN:AAC68916.1; GSPDB:GN00021; CESP:W04B5.3

A:Experimental source: strain Bristol N2; clone W04B5

C:Genetics:

A:Gene: CESP:W04B5.3

A:Map position: 3

A:Introns: 7/3; 63/3; 102/3; 124/3; 144/1; 198/3; 277/3; 301/3; 351/3; 399/1

Query Match

70.0%; Score 35; DB 2; Length 424;
Best Local Similarity Pred. No. 44;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10

Db 282 PSSVPLSTYP 291

RESULT 16

S64912

probable membrane protein YLR080W - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L2365

C:Species: Saccharomyces cerevisiae

C:Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002

C:Accession: S64912

R:Polh, T.M.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64899

A:Accession: S64912

A:Molecule type: DNA

A:Residues: 1-444 <POH>

A:Cross-references: EMBL:Z73252; NID:g1360442; PID:g1360443; GSPDB:GN00012; MIPS:YLR080W

A:Experimental source: strain S288C

C:Genetics:

A:Gene: MIPS:YLR080W

A:Cross-references: SGD:S0004070

A:Map position: 12R

C:Keywords: transmembrane protein

F:413-429/Domain: transmembrane #status predicted <TM>

Query Match

70.0%; Score 35; DB 2; Length 444;
Best Local Similarity Pred. No. 46;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PSAAVATYSP 10

Db 206 PSTRLTYNP 215

RESULT 17

S74319

RT3 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YBL0810; protein YBL103C

C:Species: Saccharomyces cerevisiae

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000

C:Accession: S74319; S45392; S45846; S59189

R:Jula, Y.; Rothmel, B.; Ethredge, J.; Bulow, R.

submitted to the EMBL Data Library, January 1996

A:Reference number: S74319

A:Accession: S74319

A:Molecule type: DNA

A:Residues: 1-486 <JIA>

A:Cross-references: EMBL:U46012; NID:g1177880; PID:g1177881

R:Obermaier, B.; Gassenhuber, C.; Piravandi, E.; Domdey, H.

submitted to the EMBL Data Library, May 1994

A:Description: Sequence analysis of a 78,6 kb segment of the left end of Saccharomyces cerevisiae

A:Reference number: S45387

A:Accession: S45392

A:Molecule type: DNA

A:Residues: 1-109, 'SWFHHLY' <OBE>

A:Cross-references: EMBL:X79489; NID:g496661; PID:g496666

A:Experimental source: strain S288C

R:Domdey, H.; Gassenhuber, H.; Obermaier, B.; Piravandi, E.

submitted to the Protein Sequence Database, August 1994

A:Reference number: S45816

A:Accession: S45846

A:Molecule type: DNA

A;Residues: 1-309, 'SWFPHLY' <DOM>
 A;Cross-references: EMBL:Z45864; MIPS:YBL103C
 A;Experimental source: strain S288C
 A;Other: Maier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
 Yeast 11, 1104-1112, 1995
 A;Title: Sequence analysis of a 78.6 kb segment of the left end of *Saccharomyces cerevisiae*
 A;Reference number: S59184; MUID:96076635; PMID:7502586
 A;Accession: S59189
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-309, 'SWFPHLY' <ORF>
 A;Cross-references: EMBL:X79489; NID:g496661; PID:g496666
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
 C;Genetics:
 A;Gene: SGP:RTG3
 A;Cross-references: SGD:S0000199; MIPS:YBL103C
 A;Map position: 21
 C;Keywords: nucleus

Query Match 70.0%; Score 35; DB 2; Length 486;
 Best Local Similarity 60.0%; Pred. No. 50;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSVALTYSP 10
 Db 214 PASVSSTYSP 223
 |||:|||||

RESULT 18
 H75349
 glycoen debranching enzyme-related protein - *Deinococcus radiodurans* (strain R1)
 C;Species: *Deinococcus radiodurans*
 C;Date: 03 Dec 1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: H75349
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: H75349
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-804 <WHI>
 A;Cross-references: GB:AF001881; GB:AF000513; NID:g6457853; PIDN:AAF09778.1; PID:g645786
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR0191
 A;Map position: 1

Query Match 70.0%; Score 35; DB 2; Length 804;
 Best Local Similarity 70.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSVALTYSP 10
 Db 42 PSASATYSP 41
 |||:|||||

RESULT 19
 S45167
 chitin synthase (EC 2.4.1.16) 2 yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: chitin-UDP acetyl-glucosaminyl-transferase 2; protein YER038w; prote
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 17-May-1994 #sequence_revision 09-Sep-1994 #text_change 20-Aug-1999
 C;Accession: S45167; S45896; A30922
 R;Silverman, S.J.
 Yeast 5, 459-467, 1989
 A;Title: Similar and different domains of chitin synthases 1 and 2 of *S. cerevisiae*: tw
 A;Reference number: S45167; MUID:90143137; PMID:2533436
 A;Accession: S45167
 A;Molecule type: DNA
 A;Residues: 1-963 <STL>

A;Cross-references: EMBL:M23865; NID:gl71219; PIDN:AAA4493.1; PID:gl71220
 R;Andre, B.; Cziepluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.
 submitted to the Protein Sequence Database, August 1994
 A;Reference number: S45893
 A;Accession: S45896
 A;Molecule type: DNA
 A;Residues: 1-963 <AND>
 A;Cross-references: EMBL:Z35907; NID:g536257; PIDN:CAA84980.1; PID:g536258; MIPS:YBR038w
 C;Genetics:
 A;Gene: SGD:CHS2
 A;Cross-references: SGD:S0000242; MIPS:YBR038w
 A;Map position: 2R
 C;Function:
 A;Description: catalyzes the alpha-1,4-glycosylation of chitin by UDP-N-acetyl D-glucosam
 C;Superfamily: chitin synthase chsA
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
 F;424-440/Domain: transmembrane #status predicted <TM1>
 F;644-660/Domain: transmembrane #status predicted <TM2>
 F;677-698/Domain: transmembrane #status predicted <TM3>
 F;708-732/Domain: transmembrane #status predicted <TM4>
 F;744-761/Domain: transmembrane #status predicted <TM5>
 F;780-796/Domain: transmembrane #status predicted <TM6>
 F;874-897/Domain: transmembrane #status predicted <TM7>
 F;902-924/Domain: transmembrane #status predicted <TM8>

Query Match 70.0%; Score 35; DB 2; Length 963;
 Best Local Similarity 70.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PSVALTYSP 10
 Db 61 PSRAALRYSP 70
 |||:|||||

RESULT 20
 S55399
 genome polyprotein - rabbit hemorrhagic disease virus (isolate BS89)
 C;Species: rabbit hemorrhagic disease virus
 A;Variety: isolate BS89
 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999
 C;Accession: S55399
 R;Rossi, C.
 submitted to the EMBL Data Library, May 1995
 A;Reference number: S55399
 A;Accession: S55399
 A;Molecule type: genomic RNA
 A;Residues: 1-2344 <ROS>
 A;Cross-references: EMBL:X87607; NID:g854640; PIDN:CAA60910.1; PID:g84641
 A;Experimental source: isolate BS89
 C;Superfamily: rabbit calicivirus RNA-directed RNA polymerase
 C;Keywords: polyprotein

Query Match 70.0%; Score 35; DB 2; Length 2344;
 Best Local Similarity 60.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSVALTYSP 10
 Db 2194 PNALITYTP 2203
 |||:|||||

RESULT 21
 G75035
 iron (iii) abc transporter, permease protein (hemu 2) PAB1535 *Pyrococcus abyssi* (stra
 C;Species: *Pyrococcus abyssi*
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug 1999 #text_change 20-Jun-2000
 C;Accession: G75035
 R;anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A;Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome str
 A;Reference number: A75001
 A;Accession: G75035
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1331 <KAM>
 A;Cross-references: GB:AJ248287; GB:AL096836; NID:G5458657; PIDN:CAB50180.1; PID:G545869
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB1535
 C;Superfamily: ferrichrome ABC transporter

Query Match 68.0%; Score 34; DB 2; Length 331;
 Best Local Similarity 66.7%; Pred. No. 54;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 PSVALTYSP 10
 |||
 Db 105 AATLALYSP 113

RESULT 22

T40466
 Probable acetyltransferase protein - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 01-Mar-2002

C;Accession: T40466

R;Lyme, M.; Rajandram, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.

Submitted to the EMBL Data Library, November 1998

Reference number: 221931

A;Accession: T40466

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-350 <LYN>

A;Cross-references: EMBL:AL034382; PIDN:CAA22289.1; GSPDB:GNO0067; SPDB:SPBC428.14

A;Experimental source: strain 972h-; cosmid C428

C;Genetics:

A;Gene: SPDB:SPBC428.14

A;Map position: 2

C;Superfamily: probable membrane protein YBR042c

Query Match 68.0%; Score 34; DB 2; Length 350;
 Best Local Similarity 60.0%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 PSVALTYSP 10
 |||
 Db 65 PTPVLTLYDP 74

RESULT 23

B82549
 Hypothetical protein XF2506 [imported] - *Xylella fastidiosa* (strain 945c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: B82549

Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing

Figure 406, 151-157, 2000

Reference: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Residues: 148215; MUID:20365717; PMID:10910147

A;Note: for a complete list of authors see reference number A5928 below

A;Accession: B82549

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-460 <STM>

A;Cross-references: GB:AE004058; GB:AE003849; NID:G9107704; PIDN:AAF85304.1; GSPDB:GN001

A;Experimental source: strain 945c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Doroty, H.; Facincani, A.P.; Ferreira, A.U.S.

Submitted to Genbank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigh

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranda, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeira, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF2506

Query Match 68.0%; Score 34; DB 2; Length 460;
 Best Local Similarity 77.8%; Pred. No. 75;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PSVALTYSP 9
 |||
 Db 135 PSVALGLYS 143

RESULT 24

OHYUCR

Natriuretic peptide receptor C precursor - human

A;Alternate names: atrial natriuretic factor clearance receptor; natriuretic peptide cle

C;Species: *Homo sapiens* (man)

C;Date: 09-Nov-1990 #sequence_revision 05-May-1995 #text_change 22-Jun-1999

C;Accession: S10150; A35896

R;Lowe, D.G.; Camerato, T.R.; Geeddel, D.V.

Nucleic Acids Res. 18, 3412, 1990

A;Title: cDNA sequence of the human atrial natriuretic peptide clearance receptor.

A;Reference number: S10150; MUID:90287735; PMID:2162522

A;Accession: S10150

A;Molecule type: mRNA

A;Residues: 1-540 <LOW>

A;Cross-references: EMBL:X52282; NID:G28705; PIDN:CAA36523.1; PID:G28706

A;Note: alternative splice form C6

R;Porter, J.G.; Arsten, A.; Fuller, F.; Miller, J.A.; Gregory, L.C.; Lewicki, J.A.

Biochem. Biophys. Res. Commun. 171, 796-803, 1990

A;Title: Isolation and functional expression of the human atrial natriuretic peptide cle

A;Reference number: A35896; MUID:9038656; PMID:2169733

A;Accession: A35896

A;Molecule type: mRNA

A;Residues: 1-475; 'SG', 477-540 <POR>

A;Cross-references: GB:M59305; NID:G178651; PIDN:AA51734.1; PID:G178652

A;Map position: 5P14-5P13

C;Superfamily: natriuretic peptide receptor C; natriuretic peptide-binding domain homolo

C;Keywords: alternative splicing; glycoprotein; homodimer; hormone receptor; transmembra

F;1-23/Domain: signal sequence #status predicted <SIG>

F;14-5/Domain: propeptide #status predicted <PRO>

F;16-540/Product: natriuretic peptide receptor C #status predicted <EXT>

F;131-462/Domain: natriuretic peptide-binding domain homology <NBP>

F;183-503/Domain: transmembrane #status predicted <TM>

F;186-293/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;108-136, 213-261/Disulfide bonds: #status experimental

F;1394/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

F;173-476/Disulfide bonds: (partial) (in splice form C6) #status experimental

C;Genetics:

A;Gene: GDB:NPR3; NPRC; ANPRC

A;Cross-references: GDB:125201; OMIM:108962

A;Map position: 5P14-5P13

C;Superfamily: natriuretic peptide receptor C; natriuretic peptide-binding domain homolo

C;Keywords: alternative splicing; glycoprotein; homodimer; hormone receptor; transmembra

F;1-23/Domain: signal sequence #status predicted <SIG>

F;14-5/Domain: propeptide #status predicted <PRO>

F;16-540/Product: natriuretic peptide receptor C #status predicted <EXT>

F;131-462/Domain: natriuretic peptide-binding domain homology <NBP>

F;183-503/Domain: transmembrane #status predicted <TM>

F;186-293/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;108-136, 213-261/Disulfide bonds: #status experimental

F;1394/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

F;173-476/Disulfide bonds: (partial) (in splice form C6) #status experimental

Query Match 68.0%; Score 34; DB 1; Length 540;
 Best Local Similarity 60.0%; Pred. No. 89;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PSVALTYSP 10
 |||
 Db 2 PSULVTTFSP 11

Db 2 PSULVTTFSP 11

RESULT 25

T37314
 probable kexin (EC 3.4.21.61) Caenorhabditis elegans (fragment)
 N/AIretrate names: Blisterase 4
 C/Species: Caenorhabditis elegans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C/Accession: T37314
 R/Thacker, C., Peters, K., Srayko, M.; Rose, A.M.
 Genes Dev. 9, 956-971, 1995
 A/Title: The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/su
 A/Reference number: 721679; MUID:95293228; PMID:7774813
 A/Accession: T37314
 A/Status: preliminary; translated from GB/EMBL/DDBU
 A/Molecule type: mRNA
 A/Residues: 1 570 <THA>
 A/Cross-references: EMBL:L29440; NID:g459702; PIDN AAA98752.1; PID:g459703
 C/Genetics:
 A/Gene: bli-4
 A/Map position: 1
 C/Keywords: alternative splicing; hydrolase; serine proteinase
 Query Match 68.0%; Score 34; DB 2; Length 570;
 Best Local Similarity 66.7%; Pred. No. 94;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 PSAVALTYS 9
 Db 8 PSSIAATTYS 16

Search completed: January 3, 2003, 13:02:32
 Job time : 6.65217 secs